

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/540,615
Source: PCT
Date Processed by STIC: 07-11-2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/540,615

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or, scientific name (Genus/species). ~~<220>-<223> section is required when <213> response is Unknown or is Artificial Sequence~~

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

4 <110> APPLICANT: CENTER FOR GENETIC ENGINEERING AND BIOTECHNOLOGY
 6 <120> TITLE OF INVENTION: RECOMBINANT HEPATITIS A VIRUS ANTIGENS PRODUCED IN PLANT CELLS.
 9 <130> FILE REFERENCE: ORF.
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/540,615
 C--> 12 <141> CURRENT FILING DATE: 2005-06-23
 14 <160> NUMBER OF SEQ ID NOS: 24
 16 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 25
 E--> 20 <212> TYPE: ADN *PLS use type DNA*
 21 <213> ORGANISM: Chimeric Sequence
 24 <220> FEATURE:
 25 <221> NAME/KEY: primer_bind
 26 <222> LOCATION: (1)..(25)
 27 <223> OTHER INFORMATION: Sequence # 1.
 28 Sequence of the oligonucleotide # 1 used for the amplification of ORF
 29 coding sequence by RT-PCR.
 32 <400> SEQUENCE: 1
 33 cttaatctag aatgaatatg tccaa
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 22
 E--> 38 <212> TYPE: ADN *Does Not Comply*
 39 <213> ORGANISM: Chimeric Sequence *Corrected Diskette Needed*
 41 <220> FEATURE:
 42 <221> NAME/KEY: primer_bind
 43 <222> LOCATION: (1)..(22)
 44 <223> OTHER INFORMATION: Sequence # 2.
 45 Sequence of the oligonucleotide # 2 used for the amplification of ORF
 46 coding sequence by RT-PCR.
 47 <400> SEQUENCE: 2
 48 gaaagaaata aaggtacctc ag
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 6685
 E--> 53 <212> TYPE: ADN *Invalid Response see item # 10 on error summary sheet.*
 54 <213> ORGANISM: Hepatitis A virus
 56 <220> FEATURE:
 57 <221> NAME/KEY: gene
 58 <222> LOCATION: Complement((1)..(6685))
 59 <223> OTHER INFORMATION: Sequence # 3.

Same error (pointing to line 38)
Same error (pointing to line 53)

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60 Nucleotide sequence coding for the HAV open reading frame (ORF) of the
 61 Cuban M2 strain.

64 <400> SEQUENCE: 3

```

65 atgaatatgt ccaaacaagg aattttccag actgttggga gtggccttga ccacatcctg 60
66 tccttggcag atattgagga agagcaaagt attcagtcctg ttgataggac tgcagtgact 120
67 ggagcttctt atttcacttc tgtggaccaa tcttcagttc atactgctga ggttggctca 180
68 caccaaattg aacctttgaa aacctctgtt gataaacctg gttctaagaa aactcagggg 240
69 gagaagtttt tcttgattca ttctgctgat tggctcacta cacatgctct ctttcatgaa 300
70 gttgcaaaat tggatgtggt gaaactgctg tacaatgagc agtttgccgt ccaagggtttg 360
71 ttgagatacc atacttatgc aagatttggc attgagattc aagttcagat aaatcccaca 420
72 ccctttcagc aaggaggact aatctgtgcc atggttcctg gtgaccaaag ttatggttca 480
73 atagcatcct tgactgttta tcctcatggt ctgttaaatt gcaatatcaa caatgtagtt 540
74 agaataaagg ttccatttat ttatactaga ggtgcttctc attttaaaga tccacagtac 600
75 ccagtttggg aattgacaat cagagtttgg tcagagtga atattggaac aggaacctca 660
76 gcttatactt cactcaatgt tttacagatt ttacagatt tggagtgtga tggattaact 720
77 cctctttcta cacagatgat gagaaatgaa tttagagtta gtactactga aaatgttgta 780
78 aatttgtcaa attatgaaga tgcaagggca aaaatgtctt ttgctttgga tcaggaagat 840
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80 tccattccaa ccttagctgc tcagtttcca ttcaatgctt cagattcagt tgggcaacaa 960
81 attaaagtta taccagtgga cccatacttt ttccagatga caaacactaa tcctgatcaa 1020
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83 gttttcgatt tccaggtttt tccaaccaa tatcattcag gtaggctgtt gttttgtttt 1140
84 gttcctggga atgagttaat agatgttact ggaattacat taaaacaggc aactactgct 1200
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88 gttgcttctc atgttagagt taatgtttat ctttcagcaa ttaatttggga atgttttgct 1440
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90 acaacagttt ctacagagca gaatgttctc gatccccaag ttggcataac aaccatgagg 1560
91 gatttaaaag ggaaagccaa taggggaaag atggatgtat caggagtga ggtacctgtg 1620
92 ggagctatta caacaattga ggatccagtt ttagcaaaga aagtacctga gacatttctc 1680
93 gaattgaagc ctggagaatc cagacataca tcagatcaca tgtctattta taaattcatg 1740
94 ggaaggtctc atttcttgtg tacttttact tttaattcaa acaataaaga gtacacattt 1800
95 ccaataactc tgtcttcgac ttctaactct cctcatggtt taccatcaac attaagggtg 1860
96 ttctttaatt tgtttcagtt gtatagagga ccattggatt tgacaattat aatcacagga 1920
97 gccactgatg tggatggtat ggcctggttt actccagtgg gccttgctgt cgacaccctt 1980
98 tgggtggaaa agaagtcagc tttgtctatt gattataaaa ctgcccttgg agctgttaga 2040
99 ttaatacaa gaagaacagg gaacattcag attagattgc catggtattc ttatttgtat 2100
100 gccgtgtctg gagcactgga tggccttggga gataagacag attctacatt tggattggtt 2160
101 tctattcaga ttgcaaatca caatcattct gatgaatatt tgtcctttag ttgttatttg 2220
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105 aaagaattga gactggaggt tgggaaacaa agaatcaaat atgctcagga agagtatatca 2460
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Output Set: N:\CRF4\07112005\J540615.raw

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112 gattttccaa atatgtctga gacagatttg tgtttcctgt tgcattggct aaatccaaag 2880
113 aaaattaatt tagcagatag aatgcttgga ttgtctggag tgcaggaaat taaagaacag 2940
114 ggtgttggaac tgatagcaga gtgtagaact ttcttgatt ctattgctgg gactttgaaa 3000
115 tctatgattt ttgggtttca ttattctgtg actgttgaaa ttataaatat tgtgctttgt 3060
116 tttattaaga gtggaatcct gctttatgtc atacaacaat tgaaccaaga tgaacactct 3120
117 cacataattg gtttggtgag agttatgaat tatgcagata ttggctgttc agtcatttca 3180
118 tgtggtaaag ttttttccaa aatgttagaa acagttttta attggcaaag ggactctaga 3240
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120 actattttta aaagttttta ggatgccata tattggttat gtacaaaatt gaaggatttt 3360
121 tatgaagtaa attatggcaa gaaaaaggat gttcttaata ttctcaaaga taaccagcaa 3420
122 aaaatagaaa aagccattga agaagcagac aatttttgca ttttgcaaag tcaagatgtg 3480
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155 gaagaaccag aggattacaa agaagcttca gttttttatc aaaataaaaat agtaggcaag 5460
156 actcagctag ttgatgactt tctagatctt gatatggcca ttacaggggc tccaggcatt 5520
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158 agagatttga tttggttggg tgaaaatggg ttactgttag gagttcaccc aagattggcc 5640
159 cagagaatct tatttaatac tgtcatgatg gaaaattgtt ctgacttaga tgttgttttt 5700

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

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162 attagttatt ttcatttgaa tccagggttt cacacagggtg ttgctattgg catagatcct 5880
163 gatagacagt gggatgaatt atttaaaaca atgataagat ttggagatgt tggctctgat 5940
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167 gggctctcctt gtacagctttt gttgaattca attattaata atattaattt gtattatgtg 6180
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169 tatggagatg atgttttgat agttttttcc agagatgttc aaattgataa tcttgacttg 6300
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171 aaaaatgtgc ctcaactgaa gccagtttca gaattgactt ttcttaaaag atcttttaaat 6420
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174 atgcatggct atgagttcta tcagaaattc tattattttg ttcagtcctg tttggagaaa 6600
175 gagatgatat aatatagact taaatcttat gattgggtgga gaattgagatt ttatgaccag 6660
176 tgtttcattt gtgacctttc atgat                                     6685

```

E--> 179 <210> SEQ ID NO: 4

180 <211> LENGTH: 40

E--> 181 <212> TYPE: **ADN** *pl's use type DNA*

182 <213> ORGANISM: Chimeric Sequence *same error*

184 <220> FEATURE:

185 <221> NAME/KEY: primer_bind

186 <222> LOCATION: (1)..(40)

187 <223> OTHER INFORMATION: Sequence # 4.

188 Sequence of the oligonucleotide # 5 used for the

189 amplification of P1-2A coding sequence by PCR.

192 <400> SEQUENCE: 4

193 ttgaattcag cttgtgaaaa taacccttct attttcctag 40

196 <210> SEQ ID NO: 5

197 <211> LENGTH: 28

E--> 198 <212> TYPE: **ADN** *same error*

199 <213> ORGANISM: Chimeric Sequence

201 <220> FEATURE:

202 <221> NAME/KEY: primer_bind

203 <222> LOCATION: (1)..(28)

204 <223> OTHER INFORMATION: Sequence # 5.

206 Sequence of the oligonucleotide # 5 used for the

207 amplification of P1-2A coding sequence by PCR.

209 <400> SEQUENCE: 5

210 cgcccggttc tagaatgaat atgtccaa 28

213 <210> SEQ ID NO: 6

214 <211> LENGTH: 2523

E--> 215 <212> TYPE: **ADN** *same error*

216 <213> ORGANISM: Hepatitis A virus

218 <220> FEATURE:

219 <221> NAME/KEY: gene

220 <222> LOCATION: Complement((1)..(2523))

221 <223> OTHER INFORMATION: Sequence # 6.

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Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

222 Nucleotide sequence coding for the structural
 223 P1-2A HAV proteins of the M2 strain.
 226 <400> SEQUENCE: 6
 227 atgaatatgt ccaaacaagg aattttccag actgttggga gtggccttga ccacatcctg 60
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 229 ggagcttctt atttcacttc tgtggaccaaa tcttcagttc atactgctga ggttggctca 180
 230 caccaaattg aacctttgaa aacctctgtt gataaacctg gttctaagaa aactcagggg 240
 231 gagaagtttt tcttgattca ttctgctgat tggctcacta cacatgctct ctttcatgaa 300
 232 gttgcaaaat tggatgtggt gaaactgctg tacaatgagc agtttgccgt ccaaggtttg 360
 233 ttgagatacc atacttatgc aagatttggc attgagattc aagttcagat aaatcccaca 420
 234 ccctttcagc aaggaggact aatctgtgcc atggttcctg gtgaccaaag ttatggttca 480
 235 atagcatcct tgactgttta tcctcatggt ctgttaaatt gcaatatcaa caatgtagtt 540
 236 agaataaagg ttccatttat ttatactaga ggtgcttatc attttaaga tccacagtac 600
 237 ccagtttggg aattgacaat cagagtttgg tcagagttga atattggaac aggaacctca 660
 238 gcttatactt cactcaatgt tttagctagg tttacagatt tggagttgca tggattaact 720
 239 cctctttcta cacagatgat gagaaatgaa tttagagtta gtactactga aaatgttgta 780
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 246 gttcctggga atgagttaat agatgttact ggaattacat taaaacaggc aactactgct 1200
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 250 gttgcttctc atgttagagt taatgtttat ctttcagcaa ttaatttggga atgttttgc 1440
 251 cctctttacc atgctatgga tgttaccaca caggttggag atgattcagg aggttttctca 1500
 252 acaacagttt ctacagagca gaatgttcct gatccccaag ttggcataac aaccatgagg 1560
 253 gatttaaaag ggaaagccaa taggggaaag atggatgtat caggagtgcg ggtacctgtg 1620
 254 ggagctatta caacaattga ggatccagtt ttacgaaaga aagtacctga gacatttcct 1680
 255 gaattgaagc ctggagaatc cagacataca tcagatcaca tgtctattta taaattcatg 1740
 256 ggaaggtctc atttcttgtg tacttttact tttaattcaa acaataaaga gtacacattt 1800
 257 ccaataactc tgtcttcgac ttctaactct cctcatgggt taccatcaac attaaggtgg 1860
 258 ttctttaatt tgtttcagtt gtatagagga ccattggatt tgacaattat aatcacagga 1920
 259 gccactgatg tggatggtat ggcctggttt actccagtgg gccttgctgt cgacaccct 1980
 260 tgggtggaaa agaagtcagc tttgtctatt gattataaaa ctgcccttgg agctgttaga 2040
 261 ttaatacaa gaagaacagg gaacattcag attagattgc catggatttc ttatttgtat 2100
 262 gccgtgtctg gagcactgga tggcttggga gataagacag attctacatt tggattgggt 2160
 263 tctattcaga ttgcaaatca caatcattct gatgaatatt tgtccttttag ttgttatttg 2220
 264 tctgtcacag agcaatcaga gttctatttc cctagagctc cattaaattc aaatgctatg 2280
 265 ttgtccactg agtccatgat gagtagaatt gcagctggag acttggagtc atcagtggat 2340
 266 gatcccagat cagaggagga cagaagattt gagagtcata tagaatgtag gaaaccatat 2400
 267 aaagaattga gactggagggt tgggaaacaa agaatcaaat atgctcagga agagttatca 2460
 268 aatgaagtgc ttccacctcc taggaaaatg aaggggttat atgcttctgg aggtgaattc 2520
 269 gat 2523

272 <210> SEQ ID NO: 7

273 <211> LENGTH: 27

E--> 274 <212> TYPE: ADM

Same error

VERIFICATION SUMMARY

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:16

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:38 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:53 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:181 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:198 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:215 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:274 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:291 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:308 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:328 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:348 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:365 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:382 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:416 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:492 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:508 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:525 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:535 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:600 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:617 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:633 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:637 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:650 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:654 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:667 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:726 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:759 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,615

DATE: 07/11/2005
TIME: 15:15:15

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07112005\J540615.raw

632 <211> LENGTH: 55
E--> 633 <212> TYPE: ADN ← Same error
634 <213> ORGANISM: Chimeric Sequence
636 <220> FEATURE:
W--> 637 <221> NAME/KEY: D_segment
638 <222> LOCATION: (1)..(54)
639 <223> OTHER INFORMATION: Sequence # 20
640 synthetic fragment modifying the 3' end of
641 the 2A protein and introduces a space-bar
642 between this one and the KDEL signal.
644 <400> SEQUENCE: 20
645 cctaggaaaa tgaagggggtt atatgcttct ggaggtgaat tcgatatcaa ggatg 55

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

```

573 attcagattg caaattacaa tcattctgat gaatatttgt ccttttagttg ttatttgtct 2160
574 gtcacagagc aatcagagtt ctatttcctt agagctccat taaattcaaa tgctatgttg 2220
575 tccactgagt ccgatgatg tagaattgca gctggagact tggagtcac agtggatgat 2280
576 cccagatcag aggaggacag aagatttgag agtcatatag aatgtaggaa accatataaa 2340
577 gaattgagac tggagggttg gaaacaaaga atcaaatatg ctcaggaaga gttatcaaat 2400
578 gaagtgcctt cacctcctag gaaaatgaag gggttatttt cacaagctga attcctgcag 2460
579 cccgggggat ccatgggaat ttcagatgat gacaatgata gtgcagtagc tgagtttttc 2520
580 cggctctttt catctggtga accatcaaat tccaagttat ctagtttttt ccaagctgtc 2580
581 actaatcaca agtggggtgc tgtgggagct gcagttggta ttcttggatt gctagtggga 2640
582 ggatggtttg tgtataagca tttttccgc aaagaggaag aaccaattcc agctgttggg 2700
583 gtttatcatg gagtgactaa gcccaaaca gtgattaaat tggatgcaga tccagtagag 2760
584 tctcagttga ctctagaaat agcaggatta gttaggaaaa atttggttca gtttggagtt 2820
585 ggtgagaaaa atggatgtgt gagatgggtc atgaatgcct taggagtga ggtgattgg 2880
586 ttgttagtac cttctcatgc ttataaaatt gaaaaggatt atgaaatgat ggagttttat 2940
587 ttcaatagag gtggaactta ctattcaatt tcagctggta atgttggtat tcaatcttta 3000
588 gatgtgggat tccaagatgt tgttctaagt aaggttccta caattcccaa gtttagagat 3060
589 attactcaac attttattaa gaaaggagat gtgcctagag ccttgaatcg cttggcaaca 3120
590 ttagtgacaa ccgttaatgg aactcctatg ttaatttctg agggaccttt aaaaatggaa 3180
591 gaaaaagcca cttatgttca taagaagaat gatggtacta cggttgattt gactgtagat 3240
592 caggcatgga gaggaaaagg tgaaggctt cctggaatgt gtggtggggc ctagtgtca 3300
593 tcaaatcagt ccatacaaaa tgcaattttg ggtattcatg ttgctggagg aaattcaatt 3360
594 cttgtggcaa agttgattac tcaagaaatg tttcaaaaaca ttgataagaa aattgaaatc 3420
595 aagctt 3426

```

598 <210> SEQ ID NO: 18

599 <211> LENGTH: 19

E--> 600 <212> TYPE: ADN

601 <213> ORGANISM: Chimeric Sequence

603 <220> FEATURE:

604 <221> NAME/KEY: sig_peptide

605 <222> LOCATION: (1)..(19)

606 <223> OTHER INFORMATION: Sequence #18.

607 Synthetic fragment corresponding to the

608 KDEL endoplasmic reticulum retention signal

609 sequence.

611 <400> SEQUENCE: 18

612 atcaaggatg aattgtaat

19

615 <210> SEQ ID NO: 19

616 <211> LENGTH: 21

E--> 617 <212> TYPE: ADN

618 <213> ORGANISM: Chimeric Sequence

620 <220> FEATURE:

621 <221> NAME/KEY: sig_peptide

622 <222> LOCATION: (1)..(21)

623 <223> OTHER INFORMATION: Sequence #19.

624 Synthetic fragment corresponding to the KDEL

625 endoplasmic reticulum retention signal sequence.

627 <400> SEQUENCE: 19

628 cgattacaat tcattccttga t

21

631 <210> SEQ ID NO: 20

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

```

520 gtcctatcaa cggactgaat catttgctct tcctcaatat ccatccc
523 <210> SEQ ID NO: 17
524 <211> LENGTH: 3426
E--> 525 <212> TYPE: ADN ← Same error.
526 <213> ORGANISM: Hepatitis A virus
528 <220> FEATURE:
529 <221> NAME/KEY: gene
530 <222> LOCATION: Complement((1)..(3426))
531 <223> OTHER INFORMATION: Sequence # 17
532     Sequence coding for the modified open reading
533     frame (?ORFm) of the Cuban M2 strain of the HAV.
534     This sequence does not have the gene coding
W--> 535     for the VP4 protein.
537 <400> SEQUENCE: 17
538 gggatggata ttgaggaaga gcaaatgatt cagtcggttg ataggactgc agtgactgga 60
539 gcttcttatt tcacttctgt ggaccaatct tcagttcata ctgctgaggt tggctcacac 120
540 caaattgaac ctttgaaaac ctctgttgat aaacctgggt ctaagaaaac tcagggggag 180
541 aagtttttct tgattcattc tgctgattgg ctactacac atgctctctt tcatgaagtt 240
542 gcaaaattgg atgtggtgaa actgctgtac aatgagcagt ttgccgtcca aggtttgttg 300
543 agataccata cttatgcaag atttggcatt gagattcaag ttcagataaa tcccacaccc 360
544 tttcagcaag gaggactaat ctgtgccatg gttcctggtg accaaagtta tggttcaata 420
545 gcatccttga ctgtttatcc tcatggctg ttaaattgca atatcaacaa tgtagttaga 480
546 ataaagggtc catttattta tactagaggt gcttatcatt ttaaagatcc acagtacca 540
547 gtttgggaat tgacaatcag agtttggta gagttgaata ttggaacagg aacctcagct 600
548 tatacttcac tcaatgtttt agctaggttt acagatttgg agttgcatgg attaactcct 660
549 ctttctacac agatgatgag aaatgaattt agagttagta ctactgaaaa tgttgtaaat 720
550 ttgtcaaatt atgaagatgc aagggcaaaa atgtcttttg ctttggatca ggaagattgg 780
551 aagtctgatc cttcccaagg tgggtggaatt aaaattactc atttcactac ctggacatcc 840
552 attccaacct tagctgctca gtttccattc aatgcttcag attcagttgg gcaacaaatt 900
553 aaagtataac cagtggagcc atacttttcc cagatgacaa acactaatcc tgatcaaaaa 960
554 tgtataacag ccttggcctc tatttgtcag atgttctgct tttggagggg agatcttgtt 1020
555 ttcgatttcc aggtttttcc aaccaaatat cattcaggta ggctgttgtt ttgttttgtt 1080
556 cctgggaatg agttaataga tgttactgga attacattaa aacaggcaac tactgctcct 1140
557 tgtgcagtga tggacattac aggagtgcag tcaaccttga gatttcgtgt tccttggatt 1200
558 tctgatacac cctatcgagt gaataggtac acgaagtcag cacatcaaaa aggtgagtat 1260
559 actgccattg ggaagcttat tgtgtattgt tataatagat tgacttctcc ttctaattgt 1320
560 gcttctcatg ttagagttaa tgtttatctt tcagcaatta atttggaatg ttttgctcct 1380
561 ctttaccatg ctatggatgt taccacacag gttggagatg attcaggagg tttctcaaca 1440
562 acagtttcta cagagcagaa tgttcctgat cccaagttg gcataacaac catgagggat 1500
563 ttaaaaggga aagccaatag gggaaaagat gatgtatcag gagtgcaggt acctgtggga 1560
564 gctattacaa caattgagga tccagtttta gcaaagaaag tacctgagac atttctgaa 1620
565 ttgaagcctg gagaatccag acatacatca gatcacatgt ctatttataa attcatggga 1680
566 aggtctcatt tcttgtgtac ttttactttt aattcaaaca ataaagagta cacatttcca 1740
567 ataactctgt cttcgacttc taatcctcct catggtttac catcaacatt aaggtggttc 1800
568 ttttaattgt ttcagttgta tagaggacca ttggatttga caattataat cacaggagcc 1860
569 actgatgtgg atggtagtgc ctggtttact ccagtgggcc ttgctgtcga cacccttgg 1920
570 gtggaaaaga agtcagcttt gtctattgat tataaaaactg cccttggagc tgttagattt 1980
571 aatacaagaa gaacagggaa cattcagatt agattgccat ggtattctta tttgtatgcc 2040
572 gtgtctggag cactggatgg cttgggagat aagacagatt ctacatttgg attggtttct 2100

```

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

```

462 tgggtggaaa agaagtcagc tttgtctatt gattataaaa ctgcccttgg agctgttaga 2040
463 tttaatacaa gaagaacagg gaacattcag attagattgc catgggtattc ttatttgtat 2100
464 gccgtgtctg gagcactgga tggcttggga gataagacag attctacatt tggattgggt 2160
465 tctattcaga ttgcaaatta caatcattct gatgaatatt tgtcctttag ttgttatttg 2220
466 tctgtcacag agcaatcaga gttctatttc cctagagctc cattaatc aaatgctatg 2280
467 ttgtccactg agtccatgat gagtagaatt gcagctggag acttggagtc atcagtggat 2340
468 gatcccagat cagaggagga cagaagattt gagagtcata tagaatgtag gaaaccatat 2400
469 aaagaattga gactggagggt tgggaaacaa agaatcaaat atgctcagga agagttatca 2460
470 aatgaagtgc ttccacctcc taggaaaatg aaggggttat tttcacaagc tgaattcctg 2520
471 cagcccgggg gatccatggg aatttcagat gatgacaatg atagtgcagt agctgagttt 2580
472 ttccggtctt ttccatctgg tgaaccatca aattccaagt tatctagttt tttccaagct 2640
473 gtcactaatc acaagtgggt tgctgtggga gctgcagttg gtattcttgg attgctagtg 2700
474 ggaggatggt ttgtgtataa gcatttttcc cgcaaagagg aagaaccaat tccagctgtt 2760
475 ggggtttatc atggagtgac taagcccaaa caagtgatta aattggatgc agatccagta 2820
476 gagtctcagt tgactctaga aatagcagga ttagttagga aaaatttggg tcagtttggg 2880
477 gtgggtgaga aaaatggatg tgtgagatgg gtcatgaatg ccttaggagt gaaggatgat 2940
478 tgggtgttag taccttctca tgcttataaa tttgaaaagg attatgaaat gatggagttt 3000
479 tatttcaata gaggtggaac ttactattca atttcagctg gtaatgttgt tattcaatct 3060
480 ttagatgtgg gattccaaga tgttgttcta atgaagttc ctacaattcc caagtttaga 3120
481 gatattactc aacattttat taagaaagga gatgtgccta gagccttgaa tcgcttgga 3180
482 acattagtga caaccgttaa tggaaactcct atgttaattt ctgagggacc tttaaaaatg 3240
483 gaagaaaaag ccacttatgt tcataagaag aatgatggta ctacggttga tttgactgta 3300
484 gatcaggcat ggagaggaaa aggtgaaggt cttcctggaa tgtgtgggtg gccctagt 3360
485 tcatcaaatc agtccatata aaatgcaatt ttgggtattc atgttgctgg aggaaattca 3420
486 attcttgtgg caaagttgat tactcaagaa atgtttcaaa acattgataa gaaaattgaa 3480
487 atcaagctt 3489

```

```

490 <210> SEQ ID NO: 15
491 <211> LENGTH: 51
E--> 492 <212> TYPE: ADN
493 <213> ORGANISM: Chimeric Sequence
495 <220> FEATURE:
496 <221> NAME/KEY: gene
497 <222> LOCATION: (1)..(51)
498 <223> OTHER INFORMATION: Sequence # 15.
499     Synthetic fragment that reverts the
500     transcription start of the vp2 protein.
502 <400> SEQUENCE: 15
503 gggatggata ttgaggaaga gcaaatgatt cagtccgttg ataggactgc a 51
506 <210> SEQ ID NO: 16
507 <211> LENGTH: 47
E--> 508 <212> TYPE: ADN
509 <213> ORGANISM: Chimeric Sequence
511 <220> FEATURE:
512 <221> NAME/KEY: gene
513 <222> LOCATION: (1)..(47)
514 <223> OTHER INFORMATION: Sequence # 16.
515     Synthetic fragment that reverts the transcription
516     start of the vp2 protein (complementary chain).
519 <400> SEQUENCE: 16

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,615

DATE: 07/11/2005
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Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07112005\J540615.raw

Same error

```

346 <210> SEQ ID NO: 11
347 <211> LENGTH: 25
E--> 348 <212> TYPE: ADN
349 <213> ORGANISM: Chimeric Sequence
351 <220> FEATURE:
352 <221> NAME/KEY: primer_bind
353 <222> LOCATION: (1)..(25)
354 <223> OTHER INFORMATION: Sequence # 11.
355     Sequence of the oligonucleotide # 11 used
356     for the amplification of 3C coding sequence by PCR
359 <400> SEQUENCE: 11
360 tctcagtcaa ctctagaaat agcag
363 <210> SEQ ID NO: 12
364 <211> LENGTH: 21
E--> 365 <212> TYPE: ADN
366 <213> ORGANISM: Chimeric Sequence
368 <220> FEATURE:
369 <221> NAME/KEY: primer_bind
370 <222> LOCATION: (1)..(21)
371 <223> OTHER INFORMATION: Sequence # 12.
372     Sequence of the oligonucleotide # 12 used for
373     the amplification of 3C coding sequence by PCR
376 <400> SEQUENCE: 12
377 ataagcttga tcaattttct t
380 <210> SEQ ID NO: 13
381 <211> LENGTH: 978
E--> 382 <212> TYPE: ADN
383 <213> ORGANISM: Hepatitis A virus
385 <220> FEATURE:
386 <221> NAME/KEY: gene
387 <222> LOCATION: Complement((1)..(978))
388 <223> OTHER INFORMATION: Sequence # 13.
389     Sequence corresponding to the region of 3ABC
390     polyprotein with proteolytic activity having
391     the selfprocessing sites mutated.
394 <400> SEQUENCE: 13
395 gaattcctgc agcccggggg atccatggga atttcagatg atgacaatga tagtgcagta 60
396 gctgagtttt tccggtcttt tccatctggt gaaccatcaa attccaagtt atctagtttt 120
397 ttccaagctg tcaactaatca caagtgggtt gctgtgggag ctgcagttgg tattcttgga 180
398 ttgctagtgg gaggatgggt tgtgtataag catttttccc gcaaagagga agaaccaatt 240
399 ccagctgttg gggtttatca tggagtgact aagcccaaac aagtgattaa attggatgca 300
400 gatccagtag agtctcagtt gactctagaa atagcaggat tagttaggaa aaatttggtt 360
401 cagtttgagg ttggtgagaa aaatggatgt gtgagatggg tcatgaatgc ctaggagtg 420
402 aaggatgatt gggtgttagt accttctcat gcttataaat ttgaaaagga ttatgaaatg 480
403 atggagtttt atttcaatag aggtggaact tactattcaa tttcagctgg taatgttggt 540
404 attcaatctt tagatgtggg attccaagat gttgttctaa tgaagggtcc tacaattccc 600
405 aagtttagag atattactca acattttatt aagaaaggag atgtgcctag agccttgaat 660
406 cgcttggcaa cattagtgc aaccgttaat ggaactccta tgtaatttc tgagggacct 720
407 ttaaaaaatgg aagaaaaagc cacttatgtt cataagaaga atgatggtac tacggttgat 780

```

RAW SEQUENCE LISTING

DATE: 07/11/2005

PATENT APPLICATION: US/10/540,615

TIME: 15:15:15

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\07112005\J540615.raw

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408 ttgactgtag atcaggcatg gagaggaaaa ggtgaaggtc ttcctggaat gtgtggtggg 840
409 gccctagtgt catcaaatca gtccatacaa aatgcaattt tgggtattca tgttgctgga 900
410 ggaaattcaa ttcttggtgc aaagttgatt actcaagaaa tgtttcaaaa cattgataag 960
411 aaaattgaaa tcaagctt 978
414 <210> SEQ ID NO: 14
415 <211> LENGTH: 2489
E--> 416 <212> TYPE: ADN same error
417 <213> ORGANISM: Hepatitis A virus
419 <220> FEATURE:
420 <221> NAME/KEY: gene
421 <222> LOCATION: Complement((1)..(3489))
422 <223> OTHER INFORMATION: Sequence # 14.
423     Nucleotide sequence CODING for the new
424     modified open reading frame (ORFm) of the
425     Cuban M2 strain.
428 <400> SEQUENCE: 14
429 atgaatatgt ccaaacaaagg aattttccag actgttggga gtggccttga ccacatcctg 60
430 tccttggcag atattgagga agagcaaatg attcagtcctg ttgataggac tgcagtgact 120
431 ggagcttctt atttcacttc tgtggaccaa tcttcagttc atactgctga ggttggctca 180
432 caccaaattg aacctttgaa aacctctggt gataaacctg gttctaagaa aactcagggg 240
433 gagaagtttt tcttgattca ttctgctgat tggctcacta cacatgctct ctttcatgaa 300
434 gttgcaaaat tggatgtggt gaaactgctg tacaatgagc agtttgccgt ccaaggtttg 360
435 ttgagatacc atacttatgc aagatttggc attgagattc aagttcagat aaatcccaca 420
436 ccctttcagc aaggaggact aatctgtgcc atggttcctg gtgaccaaag ttatggttca 480
437 atagcatcct tgactgttta tcctcatggt ctgttaaatt gcaatatcaa caatgtagtt 540
438 agaataaaag ttccatttat ttatactaga ggtgcttatt attttaaaga tccacagtac 600
439 ccagtttggg aattgacaat cagagtttgg tcagagttga atattggaac aggaacctca 660
440 gcttatactt cactcaatgt tttagctagg tttacagatt tggagttgca tggattaact 720
441 cctctttcta cacagatgat gagaaatgaa tttagagtta gtactactga aaatgttgta 780
442 aatttgtaaa attatgaaga tgcaagggca aaaatgtctt ttgctttgga tcaggaagat 840
443 tggaaagtctg atccttccca aggtggtgga attaaaatta ctcatttcac tacctggaca 900
444 tccattccaa ccttagctgc tcagtttcca ttcaatgctt cagattcagt tgggcaacaa 960
445 attaaagtta taccagtgga cccatacttt ttccagatga caaacactaa tcctgatcaa 1020
446 aaatgtataa cagccttggc ctctatttgt cagatgttct gcttttggag gggagatctt 1080
447 gttttcgatt tccaggtttt tccaaccaa tatcattcag gtaggctgtt gttttgtttt 1140
448 gttcctggga atgagttaat agatgttact ggaattacat taaaacaggc aactactgct 1200
449 ccttggtgcag tgatggacat tacaggagtg cagtcaacct tgagatttcg tgttccttgg 1260
450 atttctgata caccctatcg agtgaatagg tacacgaagt cagcacatca aaaaggtgag 1320
451 tatactgcc a ttgggaagct tattgtgtat tggtataata gattgacttc tccttctaata 1380
452 gttgcttctc atgttagagt taatgtttat ctttcagcaa ttaatttggga atgttttgct 1440
453 cctctttacc atgctatgga tgttaccaca caggttggag atgattcagg aggtttctca 1500
454 acaacagttt ctacagagca gaatgttctt gatccccaag ttggcataac aacctagagg 1560
455 gatttaaaaag ggaaaagcaa taggggaaag atggatgtat caggagtgc ggtacctgtg 1620
456 ggagctatta caacaattga ggatccagtt ttagcaaaga aagtacctga gacatttcct 1680
457 gaattgaagc ctggagaatc cagacataca tcagatcaca tgtctattta taaattcatg 1740
458 ggaaggtctc atttcttgtg tacttttact ttttaattcaa acaataaaga gtacacattt 1800
459 ccaataactc tgtcttcgac ttctaactct cctcatggtt taccatcaac attaaggtgg 1860
460 ttctttaatt tgtttcagtt gtatagagga ccattggatt tgacaattat aatcacagga 1920
461 gccactgatg tggatggtat ggcctggttt actccagtgg gccttgctgt cgacaccct 1980

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/540,615

DATE: 07/11/2005
TIME: 15:15:15

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07112005\J540615.raw

275 <213> ORGANISM: Chimeric Sequence ← Same error.
277 <220> FEATURE:
278 <221> NAME/KEY: primer_bind
279 <222> LOCATION: (1)..(27)
280 <223> OTHER INFORMATION: Sequence # 7.
281 Sequence of the oligonucleotide # 7 used for
282 the amplification of 3A coding sequence by PCR.
285 <400> SEQUENCE: 7
286 ccatgggaat ttcagatgat gacaatg 27
289 <210> SEQ ID NO: 8
290 <211> LENGTH: 26
E--> 291 <212> TYPE: ADN ← Same error
292 <213> ORGANISM: Chimeric Sequence
294 <220> FEATURE:
295 <221> NAME/KEY: primer_bind
296 <222> LOCATION: (1)..(26)
297 <223> OTHER INFORMATION: Sequence # 8.
298 Sequence of the oligonucleotide # 7 used for
299 the amplification of 3A coding sequence by PCR.
302 <400> SEQUENCE: 8
303 ggatatcggg tcttctcttt tgcggg 26
306 <210> SEQ ID NO: 9
307 <211> LENGTH: 85 ← Same error
E--> 308 <212> TYPE: ADN
309 <213> ORGANISM: Chimeric Sequence
312 <220> FEATURE:
313 <221> NAME/KEY: gene
314 <222> LOCATION: (1)..(85)
315 <223> OTHER INFORMATION: Sequence # 9.
316 Synthetic fragment coding for 3B protein
317 carrying T by C and G by C nucleotide
318 substitutions, respectively.
321 <400> SEQUENCE: 9
322 tccagctggt ggggtttatc atggagtgac taagcccaaa caagtgatta aattggatgc 60
323 agatccagta gagtctcagt tgact 85
326 <210> SEQ ID NO: 10
327 <211> LENGTH: 89 ← Same error
E--> 328 <212> TYPE: ADN
329 <213> ORGANISM: Chimeric Sequence
332 <220> FEATURE:
333 <221> NAME/KEY: gene
334 <222> LOCATION: (1)..(89)
335 <223> OTHER INFORMATION: Sequence # 10.
336 Synthetic fragment coding for 3B protein
337 carrying T by C and G by C nucleotide
338 substitutions, respectively (complementary chain).
341 <400> SEQUENCE: 10
342 ctagagtcaa ctgagactct actggatctg catccaattt aatcacttgt ttgggcttag 60
343 tcaactccatg ataaacccca acagctgga 89